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TECH CENTER 1600/2900

## SEQUENCE LISTING

&lt;110&gt; Barber, Elizabeth K

&lt;120&gt; Gene Expression Control Element DNA

&lt;130&gt; 896034605001

&lt;140&gt; US 09/966,264

&lt;141&gt; 2001-09-28

&lt;150&gt; US 60/237,079

&lt;151&gt; 2000-09-30

&lt;160&gt; 61

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 137

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 1

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Tyr Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu  
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tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95  
Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys  
15 20 25

ggt aga aat agc atg aga agc cgt gtt tga tgt taa tta att 137  
Gly Arg Asn Ser Met Arg Ser Arg Val Cys Leu Ile  
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&lt;211&gt; 996

&lt;212&gt; DNA

&lt;213&gt; human

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Val Val Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu  
1 5 10 15

taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96  
Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro  
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atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga 144  
Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly  
35 40 45

att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat 192

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Phe	Ser	Met		Thr	Pro	Val	Ala		Ser	Asn	Ile	Lys	Leu	Ile	Leu
				65						70					75
aca	aac	aac	gtg	taa	tgg	ctt	cat	taa	taa	ggc	ttt	gct	tct	tcc	tgg 288
Thr	Asn	Asn	Val		Trp	Leu	His			Gly	Phe	Ala	Ser	Ser	Trp
					80							85			
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Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu
	90					95					100				
ctg	tgt	tgt	ctt	cac	cca	gaa	atg	ggg	aat	gat	ttc	cca	aat	ggc	aaa 384
Leu	Cys	Cys	Leu	His	Pro	Glu	Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys
105					110					115					120
gaa	aca	gag	tga	tgc	tat	cta	tct	gca	cct	ttt	gta	aag	tct	gtc	ttt 432
Glu	Thr	Glu		Cys	Tyr	Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe
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ctt	tct	ctt	tgt	ttt	cca	gga	cac	aat	gta	gga	agt	ctt	ttc	cac	atg 480
Leu	Ser	Leu	Cys	Phe	Pro	Gly	His	Asn	Val	Gly	Ser	Leu	Phe	His	Met
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gca	gat	gat	ttg	ggc	aga	gcg	atg	gag	tcc	tta	gta	tca	gtc	atg	aca 528
Ala	Asp	Asp	Leu	Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr
			155					160					165		
gat	gaa	gaa	gga	gca	gaa	taa	atg	ttt	tac	aac	tcc	tga	ttc	ccg	cat 576
Asp	Glu	Glu	Gly	Ala	Glu		Met	Phe	Tyr	Asn	Ser		Phe	Pro	His
		170						175						180	
ggg	ttt	tat	aat	att	cat	aca	aca	aag	agg	att	aga	cag	taa	gag	ttt 624
Gly	Phe	Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln		Glu	Phe
			185					190						195	
aca	aga	aat	aaa	tct	ata	ttt	ttg	tga	agg	gta	gtg	gta	tta	tac	tgt 672
Thr	Arg	Asn	Lys	Ser	Ile	Phe	Leu		Arg	Val	Val	Val	Leu	Tyr	Cys
			200						205					210	
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Arg	Phe	Gln		Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys		Gln	Trp	Gln
				215					220					225	
gtt	tta	cac	gtc	tat	gca	att	gta	caa	aaa	agt	tat	aag	aaa	act	aca 768
Val	Leu	His	Val	Tyr	Ala	Ile	Val	Gln	Lys	Ser	Tyr	Lys	Lys	Thr	Thr
				230					235					240	
tgt	aaa	atc	ttg	ata	gct	aaa	taa	ctt	gcc	att	tct	tta	tat	gga	acg 816
Cys	Lys	Ile	Leu	Ile	Ala	Lys		Leu	Ala	Ile	Ser	Leu	Tyr	Gly	Thr
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His	Phe	Gly	Leu	Phe	Lys	Asn	Leu		Gln	Leu		Arg	Lys	Asn	Tyr

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Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr		
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cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960		
Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg		
285	290	295
aat agc atg aga agc cgt gtt tga tgt taa tta att 996		
Asn Ser Met Arg Ser Arg Val Cys Leu Ile		
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 Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys  
 35 40 45  
 Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln  
 50 55 60  
 Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe  
 65 70 75 80  
 Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg  
 85 90 95  
 Lys Leu His Lys Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser  
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Arg	Asn	Leu	Val	Leu	Ile	Tyr	Gly	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	
		35					40					45				
Gly	Asn	Leu	Asn	Val	Ala	Arg	His	Phe	Ser	Met	Lys	Thr	Pro	Val	Ala	
	50					55					60					
Arg	Ser	Asn	Ile	Lys	Leu	Ile	Leu	Thr	Asn	Asn	Val	Lys	Trp	Leu	His	
65				70					75						80	
Lys	Lys	Gly	Phe	Ala	Ser	Ser	Trp	Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	
			85					90						95		
Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	Leu	Cys	Cys	Leu	His	Pro	Glu	Met	
			100				105						110			
Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys	Glu	Thr	Glu	Arg	Cys	Tyr	Leu	Ser	
	115					120						125				
Ala	Pro	Phe	Val	Lys	Ser	Val	Phe	Leu	Ser	Leu	Cys	Phe	Pro	Gly	His	
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Asn	Val	Gly	Ser	Leu	Phe	His	Met	Ala	Asp	Asp	Leu	Gly	Arg	Ala	Met	
145				150					155						160	
Glu	Ser	Leu	Val	Ser	Val	Met	Thr	Asp	Glu	Glu	Gly	Ala	Glu	Lys	Met	
			165					170						175		
Phe	Tyr	Asn	Ser	Arg	Phe	Pro	His	Gly	Phe	Tyr	Asn	Ile	His	Thr	Thr	
		180						185					190			
Lys	Arg	Ile	Arg	Gln	Lys	Glu	Phe	Thr	Arg	Asn	Lys	Ser	Ile	Phe	Leu	
		195				200						205				
Arg	Arg	Val	Val	Val	Leu	Tyr	Cys	Arg	Phe	Gln	Lys	Phe	Leu	Ser	Leu	
	210					215					220					
Leu	Leu	Phe	Cys	Lys	Gln	Trp	Gln	Val	Leu	His	Val	Tyr	Ala	Ile	Val	
225				230						235					240	
Gln	Lys	Ser	Tyr	Lys	Lys	Thr	Thr	Cys	Lys	Ile	Leu	Ile	Ala	Lys	Lys	
			245					250						255		
Leu	Ala	Ile	Ser	Leu	Tyr	Gly	Thr	His	Phe	Gly	Leu	Phe	Lys	Asn	Leu	
		260					265						270			
Lys	Gln	Leu	Lys	Arg	Lys	Asn	Tyr	Lys	Gly	Lys	Arg	Lys	Lys	Arg	Asn	

275		280		285
Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn				
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305		310		315
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Cys Lys Leu Ile

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att att att ttc aac cca agt aaa agc aga gag aaa ata gcc acc tcc 96  
 Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala Thr Ser  
 20 25 30

acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg aaa tga 144  
 Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu Lys  
 35 40 45

aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc gat ggt 192  
 Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp Gly  
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Gly Arg Asn Ser Met Arg Ser Arg Val  
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Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr

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Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met	
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Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu	
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Glu Glu Gly Ala Glu	
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Phe Pro His Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln  
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Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu  
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Phe Leu Ser Leu Leu Leu Phe Cys  
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 Phe Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala  
 -60 -55 -50

acc tcc acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg -96  
 Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu  
 -45 -40 -35

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 Lys Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr  
 -30 -25 -20

tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg gat ggt 0  
 Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met Asp Gly  
 -15 -10 -5

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1 5 10 15	
taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc	96
Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro	
20 25 30	
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Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly	
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Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala His	
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Phe Ser Met Thr Pro Val Ala Ser Asn Ile Lys Leu Ile Leu	
65 70 75	
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90 95 100	
ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa	384
Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys	
105 110 115 120	
gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt	432
Glu Thr Glu Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe	
125 130 135	
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140 145 150	
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Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr	
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Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His	
170 175 180	
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Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe	
185 190 195	
aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt	672
Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys	
200 205 210	
aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag	720

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Val	Leu	His	Val	Tyr	Ala	Ile	Val	Gln	Lys	Ser	Tyr	Lys	Lys	Thr	Thr	
				230					235					240		
tgt	aaa	atc	ttg	ata	gct	aaa	taa	ctt	gcc	att	tct	tta	tat	gga	acg	816
Cys	Lys	Ile	Leu	Ile	Ala	Lys		Leu	Ala	Ile	Ser	Leu	Tyr	Gly	Thr	
			245						250					255		
cat	ttt	ggg	ttg	ttt	aaa	aat	tta	taa	cag	tta	taa	aga	aag	aat	tat	864
His	Phe	Gly	Leu	Phe	Lys	Asn	Leu		Gln	Leu		Arg	Lys	Asn	Tyr	
			260						265						270	
aaa	gga	aaa	aga	aaa	taa	cgc	aat	gga	caa	gtg	gtg	aag	ctg	tga	act	912
Lys	Gly	Lys	Arg	Lys		Arg	Asn	Gly	Gln	Val	Val	Lys	Leu		Thr	
			275						280							
cag	gtg	tgc	aca	att	atc	agg	aac	acc	cca	aaa	cca	aag	tga	ggg	aga	960
Gln	Val	Cys	Thr	Ile	Ile	Arg	Asn	Thr	Pro	Lys	Pro	Lys		Gly	Arg	
			285					290						295		
aat	agc	atg	aga	agc	cgt	gtt	tga	tgt	taa	tta	att					996
Asn	Ser	Met	Arg	Ser	Arg	Val		Cys		Leu	Ile					
			300			305										

<210> 52  
 <211> 47  
 <212> PRT  
 <213> human

<400> 52

Phe	Pro	Ile	Gln	Cys	Ile	Val	His	Gln	Arg	Ser	Ile	Gln	Glu	Phe	
1				5					10					15	
Ile	Ile	Ile	Ile	Phe	Asn	Pro	Ser	Lys	Ser	Arg	Glu	Lys	Ile	Ala	
				20					25					30	
Thr	Ser	Thr	Ile	Ala	Ser	Glu	Ala	Ser	Gln	Gln	Pro	Glu	Thr	Ala	
				35					40					45	

Leu Lys

<210> 53  
 <211> 32  
 <212> PRT  
 <213> human

<400> 53

Lys	Val	Gly	Val	Ala	Val	Met	Val	Ala	Val	Ile	Met	Val	Thr	Asp	
1				5					10					15	



Gly Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met  
 20 25 30

Val Val

<210> 54  
 <211> 1044  
 <212> DNA  
 <213> mouse

<400> 54

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gatagtaaaa gtgtagacta tacaacagaa taaatacaag tatagtaaat 150
ccaacaaagt gtgaaagggtg tgtgccatta cacatctttc tcggtgataa 200
gagccttgtc tatgaagttc tgagatgtgt taggaagatg aatcatcaat 250
ttacatttct ccccatcaaa tgacaccatg ctgatccagt attaagctaa 300
tactaacacc atgcaatgct tcattaacaa ggatttgctt cttgctagaa 350
atgggtaaaa acggactgtg gtctgtatac cttcaatgca gcttatgtgt 400
tgtcttttcc tgaaatggta atgactccca atagtggcaa ccaggggtac 450
aatacttgca cactttgtaa actctttctt tctctttggt ttccaggaca 500
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agtccttagt ttcagtcag acagatgaag aaggagcaga ataaatgttt 600
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tatggaacgc attttgggtt gtttaaaaaat ttataacagt tataaagaaa 900
gattgtaaac taaagtgtgc ttataaaaaa agtttggtta taaaaacccc 950
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ctgaggcagc acattgtttt gcattacttt agcgtgtatc atat 1044

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<210> 55

<211> 1236  
<212> DNA  
<213> human

<400> 55

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ttattattat tttcaaccca agtaaaagca gagagaaaat agccacctcc 100
accatagcct cagaagcaag ccaacagcct gaaacagctt tgaaatgaaa 150
agttgggtgtg gcggtgatgg tggcagtgat aatggtgacc gatgggtggg 200
tgctggtgat ggtagtggta gttgtga.ag gtggtgatgg tggtttgatt 250
gatagtaaaa aaaatgttcg ttaatacaag tagagagtaa gtaatcaatc 300
aatcactcat agccaagggtg gaaaagatgt atcccatcat ggaatattcc 350
tgttctgata gaaatcttgt gcttatctat ggaattcttt tgatatatat 400
ttacattggg aacctgaatg tagcttgaca tttttccatg taaacaccag 450
tagcctgatc caacattaag ctgatactaa caaacaacgt gtaatggctt 500
cattaataag gctttgcttc ttcctggaaa ctggtgaaaa atcaaacctt 550
gttgtgtaca ccctcgatgc agcttctgtg ttgtcttcac ccagaaatgg 600
ggaatgattt cccaaatggc aaagaaacag agtgatgcta tctatctgca 650
ccttttgtaa agtctgtctt tctttctctt tgttttccag gacacaatgt 700
aggaagtctt ttccacatgg cagatgattt gggcagagcg atggagtcct 750
tagtatcagt catgacagat gaagaaggag cagaataaat gttttacaac 800
tcctgattcc cgcatggttt ttataatatt catacaacaa agaggattag 850
acagtaagag tttacaagaa at.aaatcta tttttttgtg aagggtagtg 900
gtattatact gtagatttca gtagtttcta agtctgttat tgttttgtta 950
acaatggcag gttttacacg tctatgcaat tgtacaaaaa agttataaga 1000
aaactacatg taaaatcttg atagctaaat aacttgccat ttctttatat 1050
ggaacgcatt ttgggttggt taaaaattta taacagttat aaagaaagaa 1100
ttataaagga aaaagaaaat aacgcaatgg acaagtgggtg aagctgtgaa 1150
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<210> 56

<211> 303  
<212> PRT  
<213> human

<400> 56

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Leu	Ile	Tyr	Gly	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu
				20					25					30
Asn	Val	Ala	Arg	His	Phe	Ser	Met	Lys	Thr	Pro	Val	Ala	Arg	Ser
				35					40					45
Asn	Ile	Lys	Leu	Ile	Leu	Thr	Asn	Asn	Val	Lys	Trp	Leu	His	Lys
				50					55					60
Lys	Gly	Phe	Ala	Ser	Ser	Trp	Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu
				65					70					75
Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	Leu	Cys	Cys	Leu	His	Pro	Glu
				80					85					90
Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys	Glu	Thr	Glu	Arg	Cys	Tyr
				95					100					105
Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe	Leu	Ser	Leu	Cys	Phe
				110					115					120
Pro	Gly	His	Asn	Val	Gly	Ser	Leu	Phe	His	Met	Ala	Asp	Asp	Leu
				125					130					135
Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr	Asp	Glu	Glu
				140					145					150
Gly	Ala	Glu	Lys	Met	Phe	Tyr	Asn	Ser	Arg	Phe	Pro	His	Gly	Phe
				155					160					165
Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln	Lys	Glu	Phe	Thr
				170					175					180
Arg	Asn	Lys	Ser	Ile	Phe	Leu	Arg	Arg	Val	Val	Val	Leu	Tyr	Cys
				185					190					195
Arg	Phe	Gln	Lys	Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys	Lys	Gln	Trp
				200					205					210
Gln	Val	Leu	His	Val	Tyr	Ala	Ile	Val	Gln	Lys	Ser	Tyr	Lys	Lys
				215					220					225
Thr	Thr	Cys	Lys	Ile	Leu	Ile	Ala	Lys	Lys	Leu	Ala	Ile	Ser	Leu
				230					235					240
Tyr	Gly	Thr	His	Phe	Gly	Leu	Phe	Lys	Asn	Leu	Lys	Gln	Leu	Lys
				245					250					255

Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn Gly Gln Val  
 260 265 270

Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro  
 275 280 285

Lys Pro Lys Arg Gly arg Asn Ser Met Arg Ser Arg Val Arg Cys  
 290 295 300

Lys Leu Ile

<210> 57  
 <211> 111  
 <212> DNA  
 <213> human

<400> 57  
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 aaaagttggt tataaaaacc cctaaaaaca aaacaaacac acacacacac 100  
 acatacacac a 111

<210> 58  
 <211> 260  
 <212> DNA  
 <213> human

<400> 58  
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 AACATCAAAC ACGGCTTCTC ATGCTATTTT TACCTCACTT TGGTTTTGGG 100  
 GTGTTCTCTGA TAATTGTGCA CACCTGAGTT CACAGCTTCA CCACTTGTCC 150  
 ATTGCGTTAT TTTCTTTTTC CTTTATAATT CTTTCTTTTT CCTTCATAAT 200  
 TAACAGTTAT AAAGAAAGAA TTATAAAGGA AAAAGAAAAT AACGCAATGG 250  
 ACAAGTGGTG 260

<210> 59  
 <211> 17  
 <212> DNA  
 <213> human

<400> 59

gccctcattc tggagac 17

<210> 60  
 <211> 17

<212> DNA  
<213> human

<400> 60

gcggtgatgg tggcagt

17

<210> 61  
<211> 107  
<212> PRT  
<213> human

<400> 61

Met	Tyr	Pro	Ile	Met	Glu	Tyr	Ser	Cys	Ser	Asp	Arg	Asn	Leu	Val
1				5					10					15

Leu	Ile	Tyr	Gly	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu
				20					25					30

Asn	Met	Lys	Lys	Glu	Gln	Asn	Lys	Cys	Phe	Thr	Thr	Pro	Asp	Ser
				35					40					45

Arg	Met	Val	Phe	Ile	Ile	Phe	Ile	Gln	Gln	Arg	Gly	Leu	Asp	Ser
				50					55					60

Lys	Ser	Leu	Gln	Glu	Ile	Asn	Leu	Tyr	Phe	Cys	Glu	Gly	Phe	Tyr
				65					70					75

Thr	Ser	Met	Gln	Leu	Tyr	Lys	Lys	Val	Ile	Arg	Lys	Leu	His	Lys
				80					85					90

Ile	Thr	Gln	Trp	Thr	Arg	Thr	Pro	Gln	Asn	Gln	Ser	Glu	Val	Glu

				95					100					105

Ile Ala